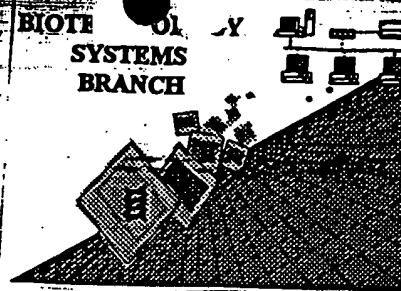


RAW SEQUENCE LISTING **ERROR REPORT**

BIOTECHNOLOGY
SYSTEMS
BRANCH



0460
APP
COPY

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/699,667

Source: OIPE

Date Processed by STIC: 11-28-00

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin30help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 3.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
<http://www.uspto.gov/web/offices/pac/checker>

NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

- ☒ 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to these regulations, published at 1114 OG 29, May 15, 1990 and at 55 FR 18230, May 1, 1990.
- ☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).
- ☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).
- ☒ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked-up "Raw Sequence Listing."
- ☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).
- ☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).
- ☐ 7. Other: _____

Applicant Must Provide:

- ☒ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".
- ☒ An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.
- ☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216

For CRF Submission Help, call (703) 308-4212

PatentIn Software Program Support (SIRA)

Technical Assistance.....703-287-0200

To Purchase PatentIn Software.....703-306-2600

PLEASE RETURN A COPY OF THIS NOTICE WITH YOUR RESPONSE

Sequence Listing Error

ary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER:

09/699,567

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 ☐ Wrapped Aminos The amino acid number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 ☐ Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 ☐ Misaligned Amino Acid Numbering The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 ☐ Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 ☐ Variable Length Sequence(s) _____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
- 7 ☐ PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 8 ☐ Skipped Sequences (OLD RULES) Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence.
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s)
- 9 ☐ Skipped Sequences (NEW RULES) Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 10 ☒ Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 ☐ Use of <213>Organism (NEW RULES) Sequence(s) _____ are missing this mandatory field or its response.
- 12 ☐ Use of <220>Feature (NEW RULES) Sequence(s) ____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 ☐ PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other means to copy file to floppy disk.

OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/699,667

DATE: 11/27/2000
TIME: 09:30:12Input Seq: N:\COPIES\EBONY\09699667.txt
Output Seq: N:\CRF3\11282000\I699667.rawDoes Not Comply
Corrected Diskette Needed

```

5 <110> APPLICANT: Bioradalt, Jean-Pierre
6   Ananyorovich, Sigrart
7   Latentia, Daniel
8   University of Stockholm
15 <120> TITLE: ENZYME: Nucleic Acid Enzyme for RNA Cleavage
19 <130> FILE REFERENCE: 77475-12
C--> 23 <140> CURRENT APPLICATION NUMBER: US/09/699,667
25 <141> CURRENT PUBLICATION DATE: 2000-1-30
29 <150> PRIOR APPLICATION NUMBER: PCT/CA99/00391
31 <151> PRIOR FILING DATE: 1999-04-29
35 <152> PRIOR APPLICATION NUMBER: CA 2,230,203
37 <153> PRIOR FILING DATE: 1998-01-29
41 <160> NUCLEIC ACID SEQUENCE: 54
45 <170> SOFTWARE: Patent Ver. 2.0
49 <210> SEQ ID NO: 1
51 <211> LENGTH: 11
53 <212> TYPE: RNA
55 <213> ORGANISM: Artificial Sequence
59 <220> FEATURE:
61 <223> OTHER INFORMATION: Description of Artificial Sequence: nucleotide
63   sequence represented by nucleotides or a
65   combination of nucleotides and
67   deoxyribonucleotides
71 <400> SEQUENCE:
W--> 76 nnrhgnnnnn n 11
77 <210> SEQ ID NO: 2
79 <211> LENGTH: 11
81 <212> TYPE: RNA
83 <213> ORGANISM: Artificial Sequence
85 <220> FEATURE:
89 <223> OTHER INFORMATION: Description of Artificial Sequence: nucleotide
91   sequence represented by nucleotides or a
93   combination of nucleotides and
95   deoxyribonucleotides
99 <400> SEQUENCE:
W--> 101 rrrhgnnnnn n 11
105 <210> SEQ ID NO: 3
107 <211> LENGTH: 11
109 <212> TYPE: RNA
111 <213> ORGANISM: Artificial Sequence
115 <220> FEATURE:
117 <223> OTHER INFORMATION: Description of Artificial Sequence: nucleotide
119   sequence represented by nucleotides or a
121   combination of nucleotides and
123   deoxyribonucleotides
127 <400> SEQUENCE:
W--> 128 gggcgnnnnn n 11

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Missing Mandatory
2207 to 2237 features
to explain the "n's"
in the sequences.
see #10 on the
Error Summary
Sheet.

RAW SEQUENCE LISTING

PATENT APPLICATION US/09/699,667

DATE: 11/26/2009

TIME: 09:30:27

Input Set: N:\COPIES\EBONY\09699667.txt

Output Set: N:\CRF3\11282000\I699667.raw

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153 <210> SEQ ID NO: 4
155 <211> LENGTH: 11
157 <212> TYPE: RNA
159 <213> ORGANISM: Artificial Sequence
161 <220> FEATURE:
163 <223> OTHER INFORMATION: Description of Artificial Sequence: nucleotide
165 sequence comprised of ribonucleotides or a
167 combination of ribonucleotides and
169 deoxyribonucleotides
171 <400> SEQUENCE:
W--> 157 gggcgnnhnn n 11
161 <210> SEQ ID NO: 5
163 <211> LENGTH: 11
165 <212> TYPE: RNA
167 <213> ORGANISM: Artificial Sequence
169 <220> FEATURE:
171 <223> OTHER INFORMATION: Description of Artificial Sequence: nucleotide
173 sequence comprised of ribonucleotides or a
175 combination of ribonucleotides and
177 deoxyribonucleotides
179 <400> SEQUENCE:
W--> 185 gggugnnnnnn n 11
189 <210> SEQ ID NO: 6
191 <211> LENGTH: 11
193 <212> TYPE: RNA
195 <213> ORGANISM: Artificial Sequence
197 <220> FEATURE:
201 <223> OTHER INFORMATION: Description of Artificial Sequence: nucleotide
203 sequence comprised of ribonucleotides or a
205 combination of ribonucleotides and
207 deoxyribonucleotides
211 <400> SEQUENCE:
W--> 213 gggugnnncnn nn 12
217 <210> SEQ ID NO: 7
219 <211> LENGTH: 11
221 <212> TYPE: RNA
223 <213> ORGANISM: Artificial Sequence
225 <220> FEATURE:
229 <223> OTHER INFORMATION: Description of Artificial Sequence: nucleotide
231 sequence comprised of ribonucleotides or a
233 combination of ribonucleotides and
235 deoxyribonucleotides
239 <400> SEQUENCE:
W--> 241 aaacgnnnnnn n 11
245 <210> SEQ ID NO: 8
247 <211> LENGTH: 11
249 <212> TYPE: RNA
251 <213> ORGANISM: Artificial Sequence
255 <220> FEATURE:

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Missing mandatory
 2207 to 2237 feature
 to explain "n's"
 in the sequences

RAW SEQUENCE LISTING

PATENT: EP1171100 US/09/699,667

DATE: 11/24/2006

TIME: 09:17:12

Input Seq: N:\COPIES\EBONY\09699667.txt

Output Seq: N:\CRF3\11282000\1699667.raw

257 <213> OTHER INFORMATION: Description of Artificial Sequence: synthetic
 259 sequence comprised of ribonucleotides or a
 261 combination of ribonucleotides and
 263 deoxyribonucleotides
 265 <100> SEQUENCE: 8
 W--> 269 yhrhgnnnnn n > Same
 271 <210> SEQ ID NO: 11 refer to p. 2
 273 <211> LENGTH: 11
 275 <212> TYPE: RNA
 277 <213> ORGANISM: Artificial Sequence
 283 <220> FEATURE:
 285 <223> OTHER INFORMATION: Description of Artificial Sequence: synthetic RNA
 287 sequence
 291 <100> SEQUENCE:
 293 qggcgagucg g 11
 297 <210> SEQ ID NO: 12
 299 <211> LENGTH: 10
 301 <212> TYPE: RNA
 303 <213> ORGANISM: Artificial Sequence
 307 <220> FEATURE:
 309 <223> OTHER INFORMATION: Description of Artificial Sequence: synthetic RNA
 311 sequence
 315 <100> SEQUENCE:
 317 qggcgagucg 10
 321 <210> SEQ ID NO: 13
 323 <211> LENGTH: 11
 325 <212> TYPE: RNA
 327 <213> ORGANISM: Artificial Sequence
 331 <220> FEATURE:
 333 <223> OTHER INFORMATION: Description of Artificial Sequence: synthetic RNA
 335 sequence
 339 <100> SEQUENCE:
 341 qggcgagucg g 11
 345 <210> SEQ ID NO: 14
 347 <211> LENGTH: 11
 349 <212> TYPE: RNA
 351 <213> ORGANISM: Artificial Sequence
 355 <220> FEATURE:
 357 <223> OTHER INFORMATION: Description of Artificial Sequence: synthetic RNA
 359 sequence
 363 <100> SEQUENCE:
 365 qggcgagucg g 11
 369 <210> SEQ ID NO: 15
 371 <211> LENGTH: 11
 373 <212> TYPE: RNA
 375 <213> ORGANISM: Artificial Sequence
 379 <220> FEATURE:
 381 <223> OTHER INFORMATION: Description of Artificial Sequence: synthetic RNA
 383 sequence

RAW SEQUENCE LISTING

BANKI APPLICATIO: US/09/699,667

Date: 11/25/2000

Time: 09:26:12

Input Seq.: N:\COPIES\EBONY\09699667.txt

Output Seq.: N:\CRF3\11282000\I699667.raw

```

517 <212> TYPE: RNA
518 <213> ORGANISM: Artificial Sequence
523 <210> LENGTH: 11
525 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic RNA
527     sequence
531 <400> SEQUENCE:
533 gggcggggcggc
537 <210> SEQ ID NO: 20
539 <211> LENGTH: 11
541 <212> TYPE: RNA
543 <213> ORGANISM: Artificial Sequence
545 <220> FEATURE
549 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic RNA
551     sequence
555 <400> SEQUENCE:
557 gggcggggcggc
561 <210> SEQ ID NO: 21
563 <211> LENGTH: 11
565 <212> TYPE: RNA
567 <213> ORGANISM: Artificial Sequence
571 <220> FEATURE
573 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic RNA
575     sequence
579 <400> SEQUENCE:
581 gggcggggcggc
583 <210> SEQ ID NO: 22
587 <211> LENGTH: 11
589 <212> TYPE: RNA
591 <213> ORGANISM: Artificial Sequence
595 <220> FEATURE
597 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic RNA
599     sequence
603 <400> SEQUENCE:
605 gggcggggcggc
609 <210> SEQ ID NO: 23
611 <211> LENGTH: 11
613 <212> TYPE: RNA
615 <213> ORGANISM: Artificial Sequence
619 <220> FEATURE
621 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic RNA
623     sequence
627 <400> SEQUENCE:
629 gggcggggcggc
633 <210> SEQ ID NO: 24
635 <211> LENGTH: 11
637 <212> TYPE: RNA
639 <213> ORGANISM: Artificial Sequence
643 <220> FEATURE
645 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic RNA

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VERIFICATION SUMMARY

DATE: 11/28/2000

TIME: 11:28 AM

Input File: N:\COPIES\EBONY\09699667.txt

Output File: N:\CRF3\11282000\1699667.raw

1:123 H:250 W: Current Application Number 1:1105 Replaced Current Application Number
 1:123 H:250 W: Mandator: Feature missing. 221a not found for SFG ID=1
 1:123 H:250 W: Mandator: Feature missing. 222a not found for SFG ID=1
 1:123 H:310 W: (46) "a" or "b" used. Feature required. for SFG ID=1
 1:101 H:250 W: Mandator: Feature missing. 221 not found for SFG ID=1
 1:101 H:250 W: Mandator: Feature missing. 222a not found for SFG ID=1
 1:101 H:340 W: (46) "a" or "b" used. Feature required. for SFG ID=1
 1:129 H:250 W: Mandator: Feature missing. 221 not found for SFG ID=1
 1:129 H:250 W: Mandator: Feature missing. 222a not found for SFG ID=1
 1:129 H:310 W: (46) "a" or "b" used. Feature required. for SFG ID=1
 1:157 H:250 W: Mandator: Feature missing. 221 not found for SFG ID=1
 1:157 H:250 W: Mandator: Feature missing. 222a not found for SFG ID=1
 1:157 H:340 W: (46) "a" or "b" used. Feature required. for SFG ID=1
 1:140 H:250 W: Mandator: Feature missing. 221 not found for SFG ID=1
 1:140 H:250 W: Mandator: Feature missing. 222a not found for SFG ID=1
 1:140 H:340 W: (46) "a" or "b" used. Feature required. for SFG ID=1
 1:213 H:250 W: Mandator: Feature missing. 221 not found for SFG ID=1
 1:213 H:250 W: Mandator: Feature missing. 222a not found for SFG ID=1
 1:213 H:340 W: (46) "a" or "b" used. Feature required. for SFG ID=1
 1:241 H:250 W: Mandator: Feature missing. 221a not found for SFG ID=1
 1:241 H:250 W: Mandator: Feature missing. 222a not found for SFG ID=1
 1:241 H:340 W: (46) "a" or "b" used. Feature required. for SFG ID=1
 1:269 H:250 W: Mandator: Feature missing. 221 not found for SFG ID=1
 1:269 H:250 W: Mandator: Feature missing. 222a not found for SFG ID=1
 1:269 H:340 W: (46) "a" or "b" used. Feature required. for SFG ID=1